because of the poor surveillance systems for recording animal casualities. Most of the reported animal cases were in domestic goats and only a lesser number were in domestic cows and dogs. In addition, two cases of deaths in humans and eight cases of deaths in animals, which were attributed to rabies virus infection had history of stray dog bites. Among the animal deaths due to rabies, there were five goats, two cows and one domestic dog.

Conclusion: Unless the local civic bodies undertake adequate measures to control the numbers of stray dogs, changing the public perception as well as opinion against the mass killings will remain an uphill task.

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Predominance of "atypical" enteroaggregative escherichia coli among human, animal, foods and associated environmental sources

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Background: Infectious diarrhoea particularly due to pathogenic bacteria is a major health problem in developing countries, including India. Despite significant reports of diarrhoeagenic *Escherichia coli* (DEC) pathotypes across the globe, there is paucity of studies which reveal their relatedness with respect to their isolation from different sources. This present study determines isolation and identification of DEC pathotypes from different sources, their genetic characterization and antibiogram sensitivity profiling.

Methods & Materials: A total of 336 samples comprising of diarrhoeic stool samples from infants (n = 103), young animals (n = 106), foods and associated environmental sources (n = 127) were screened for *E. coli*. The identified *E. coli* were confirmed as DEC pathotypes by using PCR based assays. These isolates were further studied for their genetic diversity using Pulse Field Gel Electrophoresis (PFGE) subtyping tool and their antibiogram profile was determined against seven commonly used drugs.

Results: Of the four DEC pathotypes investigated, Enteroaggregative *E. coli* (EAEC) was found to be the predominant pathogen with an isolation rate of 16.50% from infants, 17.92% from young animals and 10.24% from foods and environmental sources. These EAEC isolates, on further characterization revealed predominance of 'atypical' EAEC, with an isolation rate of 10.68% from infants, 15.09% from young animals and 10.24% from foods and associated environmental sources. On PFGE analysis, discrimination was also evident within DEC pathotypes, as only closely related EAEC isolates clustered together irrespective of their source of isolation. Further, higher antibiotic resistance pattern was observed among the isolated DEC pathotypes as almost 86.44% of isolates were found to be resistant against ≥3 tested drugs.

Conclusion: EAEC pathotype in particular 'atypical' strains were found to be the predominant pathogen. On PFGE analysis, sharing and circulation of EAEC isolates between human and animal, including foods and associated environmental sources was evident. Besides this, an alarming antimicrobial resistance profile was observed for majority of the recovered DEC pathotype isolates.

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Development of safe, effective and immunogenic vaccine candidate for diarrheagenic Escherichia coli main pathotypes in mouse model

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Background: Glanders is a highly contagious and fatal zoonotic disease primarily of horses, mules and may occur in felids in wild fields. At once time, *B.mallei* infection occurred worldwide, but over last 100 years occurrence decreased and many parts of world has been eradicated. However, sporadic cases of glanders are still registering in Far East, South America, North Africa, Middle East and Asia. In Mongolia, major glanders outbreaks were reported during the middle of last Century and due to specific measures, the prevalence was decreased to 0.05% by the end of 1980s. During the last decade, has been detecting sporadic cases and glanders likely re-emerging in Mongolia. The present study aimed to conduct the risk-based survey and identify *B.mallei* by conventional and molecular methods and identify a course of re-introduction of *B.mallei*.

Methods & Materials: Risk-based survey was conducted in Central part of Mongolia from 2014 to 2015. A total of 809 horses were tested by mallein test and CFT. Tissue samples from positive reactors were subjected for bacteriological examination and isolates were characterized by conventional and molecular methods, such as PCR, immunohistochemistry and etc. PCR performed using primers based on nucleotide difference in the 23S rDNA between *B.mallei* and *B.pseudomallei*, described previously elsewhere.

Results: Several cases of glanders, with clinical symptoms were reported and were conducted risk based surveys in outbreak areas. Of the 809 horses, 9 were positive by mallein test and 12 by CFT. From pathological samples were isolated 6 Gram negative, non-motile rods suspicious for *B.mallei.* These isolates, by PCR with primers specific for *B.malei* and *B.pseudomallei* were positive, and with *B.mallei* specific antisense primer, sense primer specific for *B.cepacia, B.vietnamese, B.mallei* and *B.pseudomallei* and competitive oligonucleotide probe for other *Burkholderia*, except *B.mallei* were

positive for *B.mallei*. Beside of these, in Gimza stained tissue sections were observed beaded bacterium, by immunohistochemistry were detected *B.mallei*.

Conclusion: Equine glanders cases, with clear symptoms, isolation and identification of *B.mallei* are indicating that glanders is re-emerging with potential risks on public health in Mongolia.

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Mozambique experience in implementing One Health Surveillance as an innovative tool to understand the risk of spillover of emerging and zoonotic infections between wildlife and humans

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Background: Zoonotic diseases are in the forefront position of emerging diseases, accounting for 70% of emerging diseases worldwide as a consequence of rapid deforestation, intense globalization, unplanned urbanization and global warming. Mozambique is a vast country, where rapid and unplanned urbanization is common, posing the risk for spill over of diseases from animals to humans. In 2012, Ministry of Health in collaboration with Faculty of Veterinary from Eduardo Mondlane University and Biotechnology Center established the first one health sentinel site to conduct research and surveillance in the interface between wildlife and humans.

Methods & Materials: The One Health sentinel surveillance site was established in Caia District, a rural area situated in Zambeze valley in the central part of the country. This district was selected because of the following characteristics, i) intense contact between humans and wildlife, ii) high vulnerability for flooding, iii) abundance of domestic animals such as cattle, pigs and poultry, and also abundance of breeding places for mosquitoes. The one health sentinel surveillance in Caia comprised three key pillars, i) surveillance of zoonotic diseases in febrile patients attended at the local district hospital, ii) surveillance of zoonotic diseases in cattle, pigs, poultry and micro mammals (bats and rodents) and iii) entomologic investigation mostly in mosquitoes and ticks.

Results: We assessed the following indicators: number of post graduation students involved, number of projects initiated, number samples collected, number of report generated and number of manuscripts published. A total of 2 PhD students and 4 Msc students from different disciplines, such as entomologists, biologists, veterinarians, medical doctors and epidemiologists are conducting their thesis in this site. An estimated 1000 serum samples were collected from febrile patients. Mosquitoes were collected as part two PhD thesis. Two project that will investigate zoonosis in poultry and cattle will start in February 2016.

Conclusion: After two years of implementation of this project, we conclude that establishment of One Health surveillance sites represents a strong platform to conduct transdisciplinary research combining human, veterinary and entomological data, so that to improve our knowledge on the risk of spillover of zoonotic diseases.

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Study of antibody dynamics in horses vaccinated against West Nile Virus (WNV)

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Background: WNV is an RNA virus belonging to *Flaviviridae* family, transmitted by mosquitoes, causing zoonosis. Humans and horses are dead-end hosts. To date, there is no cure for the disease. The prevention can be achieved minimizing the exposure to the vector or through vaccination in equine species. In Italy, two vaccines are authorized: the "Equip WNV - Pfizer" (inactivated vaccine, VM-2 strain) and the "Proteq West Nile - Merial" (recombinant canarypox virus, vCP2017 strain, that expresses the WNV prM/prE genes). Both vaccines protect against WNV lineages 1 and 2 strains. No vaccination is available for humans. Aim of this research was the study of the dynamic of antibodies in sera of vaccinated horses.

Methods & Materials: Two groups, each consisting of 20 healthy horses, serological negative to WNV, were submitted to vaccination (booster after 28 days) using authorized vaccines. After vaccination, horses were examined to evaluate the immune response from 0 to 365 days after vaccination (DAV). IgG were detected through the kit ELISA: ID Screen West Nile Competition Multi-species – ID.vet. IgM were detected using the kit ELISA: West Nile Virus IgM Antibody Test - IDEXX. All sera were tested by serum neutralization (SN) test according to the Manual of Diagnostic Tests and Vaccines for Terrestrial Animals (OIE, 2013).

Results: Data relating to IgG response showed that Pfizer vaccine induced an earlier immune response compared to the Merial one (100% of positive animals at 18° vs 38° DAV). Both vaccines produced appropriate levels of IgG for one year. SN results showed that Merial vaccine stimulated long-lasting and more intense response compared to Pfizer one (65% vs 21%). Horses treated with Merial